

Joost Snijder

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

4,560
citations

172386

29
h-index

233338

45
g-index

55
all docs

55
docs citations

55
times ranked

7759
citing authors

#	ARTICLE	IF	CITATIONS
1	Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. <i>Cell</i> , 2019, 176, 1026-1039.e15.	13.5	558
2	Tectonic conformational changes of a coronavirus spike glycoprotein promote membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11157-11162.	3.3	501
3	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	9.0	452
4	Glycan shield and epitope masking of a coronavirus spike protein observed by cryo-electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 899-905.	3.6	366
5	Induction of Potent Neutralizing Antibody Responses by a Designed Protein Nanoparticle Vaccine for Respiratory Syncytial Virus. <i>Cell</i> , 2019, 176, 1420-1431.e17.	13.5	339
6	Studying 18â€¦MDa Virus Assemblies with Native Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 4020-4023.	7.2	164
7	Defining the Stoichiometry and Cargo Load of Viral and Bacterial Nanoparticles by Orbitrap Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2014, 136, 7295-7299.	6.6	134
8	Glycan Shield and Fusion Activation of a Deltacoronavirus Spike Glycoprotein Fine-Tuned for Enteric Infections. <i>Journal of Virology</i> , 2018, 92, .	1.5	124
9	Resolving heterogeneous macromolecular assemblies by Orbitrap-based single-particle charge detection mass spectrometry. <i>Nature Methods</i> , 2020, 17, 395-398.	9.0	121
10	Boundaries of Mass Resolution in Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 906-917.	1.2	111
11	Structures of the cyanobacterial circadian oscillator frozen in a fully assembled state. <i>Science</i> , 2017, 355, 1181-1184.	6.0	106
12	An Antibody Targeting the Fusion Machinery Neutralizes Dual-Tropic Infection and Defines a Site of Vulnerability on Epstein-Barr Virus. <i>Immunity</i> , 2018, 48, 799-811.e9.	6.6	104
13	Self-Sorting of Foreign Proteins in a Bacterial Nanocompartment. <i>Journal of the American Chemical Society</i> , 2014, 136, 3828-3832.	6.6	100
14	Adeno-associated virus capsid assembly is divergent and stochastic. <i>Nature Communications</i> , 2021, 12, 1642.	5.8	99
15	Structural basis of myelin-associated glycoprotein adhesion and signalling. <i>Nature Communications</i> , 2016, 7, 13584.	5.8	94
16	Bacterial encapsulins as orthogonal compartments for mammalian cell engineering. <i>Nature Communications</i> , 2018, 9, 1990.	5.8	88
17	Adenovirus Composition, Proteolysis, and Disassembly Studied by In-depth Qualitative and Quantitative Proteomics. <i>Journal of Biological Chemistry</i> , 2014, 289, 11421-11430.	1.6	81
18	Integrin and Defensin Modulate the Mechanical Properties of Adenovirus. <i>Journal of Virology</i> , 2013, 87, 2756-2766.	1.5	76

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19	An antibody against the F glycoprotein inhibits Nipah and Hendra virus infections. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 980-987.	3.6	69
20	Vitrification after multiple rounds of sample application and blotting improves particle density on cryo-electron microscopy grids. <i>Journal of Structural Biology</i> , 2017, 198, 38-42.	1.3	68
21	Analytical Approaches for Size and Mass Analysis of Large Protein Assemblies. <i>Annual Review of Analytical Chemistry</i> , 2014, 7, 43-64.	2.8	62
22	Assembly and Mechanical Properties of the Cargo-Free and Cargo-Loaded Bacterial Nanocompartment Encapsulin. <i>Biomacromolecules</i> , 2016, 17, 2522-2529.	2.6	62
23	Insight into cyanobacterial circadian timing from structural details of the KaiB–KaiC interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1379-1384.	3.3	61
24	Self-assembly and characterization of small and monodisperse dye nanospheres in a protein cage. <i>Chemical Science</i> , 2014, 5, 575-581.	3.7	50
25	Structural Transitions and Energy Landscape for Cowpea Chlorotic Mottle Virus Capsid Mechanics from Nanomanipulation in Vitro and in Silico. <i>Biophysical Journal</i> , 2013, 105, 1893-1903.	0.2	47
26	Multimerization- and glycosylation-dependent receptor binding of SARS-CoV-2 spike proteins. <i>PLoS Pathogens</i> , 2021, 17, e1009282.	2.1	42
27	Examining the Heterogeneous Genome Content of Multipartite Viruses BMV and CCMV by Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1000-1009.	1.2	41
28	Human plasma IgG1 repertoires are simple, unique, and dynamic. <i>Cell Systems</i> , 2021, 12, 1131-1143.e5.	2.9	37
29	Mass Spectrometry-Based Structural Virology. <i>Analytical Chemistry</i> , 2021, 93, 620-640.	3.2	36
30	Architecture of a dsDNA Viral Capsid in Complex with Its Maturation Protease. <i>Structure</i> , 2014, 22, 230-237.	1.6	34
31	Germline VRC01 antibody recognition of a modified clade C HIV-1 envelope trimer and a glycosylated HIV-1 gp120 core. <i>ELife</i> , 2018, 7, .	2.8	32
32	Structural Analysis of a Temperature-Induced Transition in a Viral Capsid Probed by HDX-MS. <i>Biophysical Journal</i> , 2017, 112, 1157-1165.	0.2	28
33	Mass Spectrometry-Based <i>De Novo</i> Sequencing of Monoclonal Antibodies Using Multiple Proteases and a Dual Fragmentation Scheme. <i>Journal of Proteome Research</i> , 2021, 20, 3559-3566.	1.8	27
34	The Cleaved N-Terminus of pVI Binds Peripentonal Hexons in Mature Adenovirus. <i>Journal of Molecular Biology</i> , 2014, 426, 1971-1979.	2.0	25
35	Assessment of genome packaging in AAVs using Orbitrap-based charge-detection mass spectrometry. <i>Molecular Therapy - Methods and Clinical Development</i> , 2022, 24, 40-47.	1.8	25
36	Cryo-EM structure of coronavirus-HKU1 haemagglutinin esterase reveals architectural changes arising from prolonged circulation in humans. <i>Nature Communications</i> , 2020, 11, 4646.	5.8	24

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37	Frequency chasing of individual megadalton ions in an Orbitrap analyser improves precision of analysis in single-molecule mass spectrometry. <i>Nature Chemistry</i> , 2022, 14, 515-522.	6.6	24
38	Fluctuating Nonlinear Spring Model of Mechanical Deformation of Biological Particles. <i>PLoS Computational Biology</i> , 2016, 12, e1004729.	1.5	17
39	Antigenic structure of the human coronavirus OC43 spike reveals exposed and occluded neutralizing epitopes. <i>Nature Communications</i> , 2022, 13, .	5.8	12
40	Template-Based Assembly of Proteomic Short Reads For <i>De Novo</i> Antibody Sequencing and Repertoire Profiling. <i>Analytical Chemistry</i> , 2022, 94, 10391-10399.	3.2	12
41	Fluoxetine targets an allosteric site in the enterovirus 2C AAA+ ATPase and stabilizes a ring-shaped hexameric complex. <i>Science Advances</i> , 2022, 8, eabj7615.	4.7	11
42	Conformational landscape and pathway of disulfide bond reduction of human alpha defensin. <i>Protein Science</i> , 2015, 24, 1264-1271.	3.1	7
43	The Kai-Protein Clock "Keeping Track of Cyanobacteria's Daily Life. <i>Sub-Cellular Biochemistry</i> , 2019, 93, 359-391.	1.0	5
44	Structural Studies of Coronavirus Fusion Proteins. <i>Microscopy and Microanalysis</i> , 2019, 25, 1300-1301.	0.2	4
45	Human Plasma IgG1 Repertoires are Simple, Unique, and Dynamic. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4